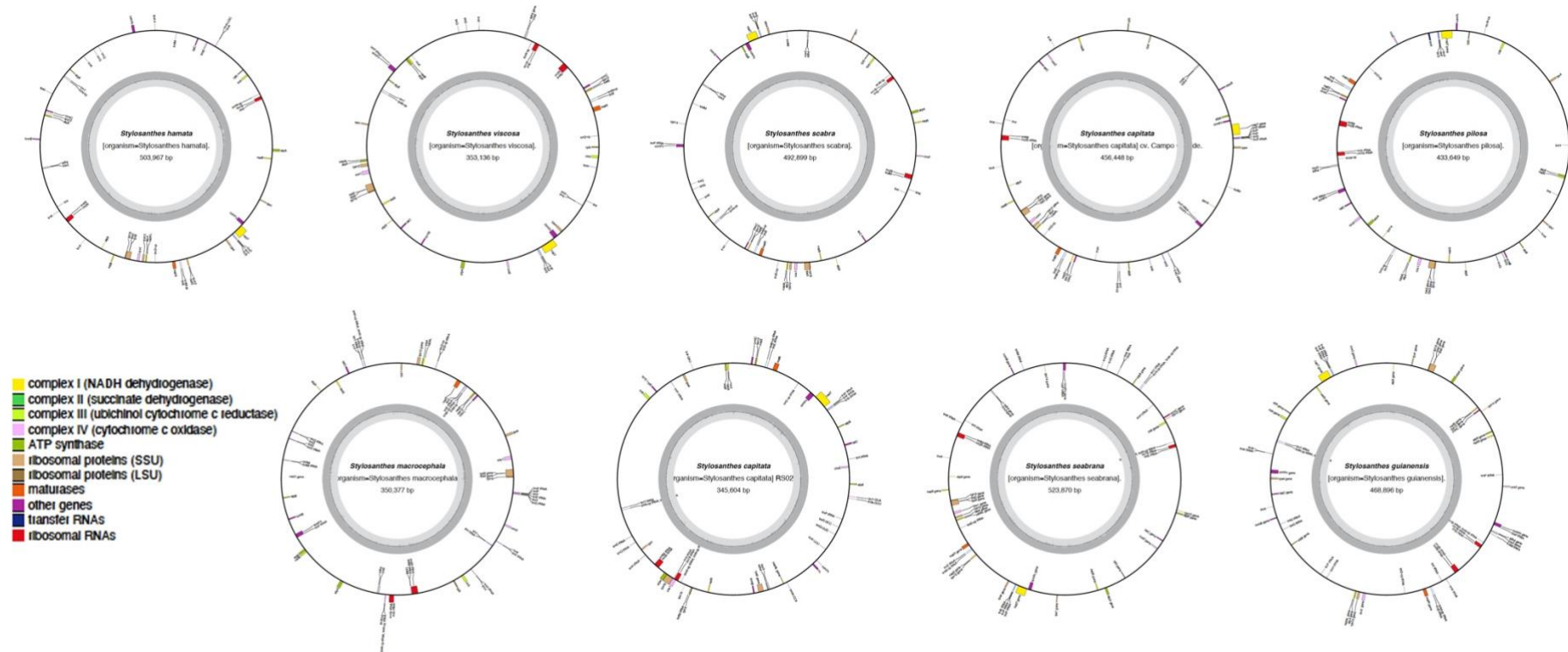
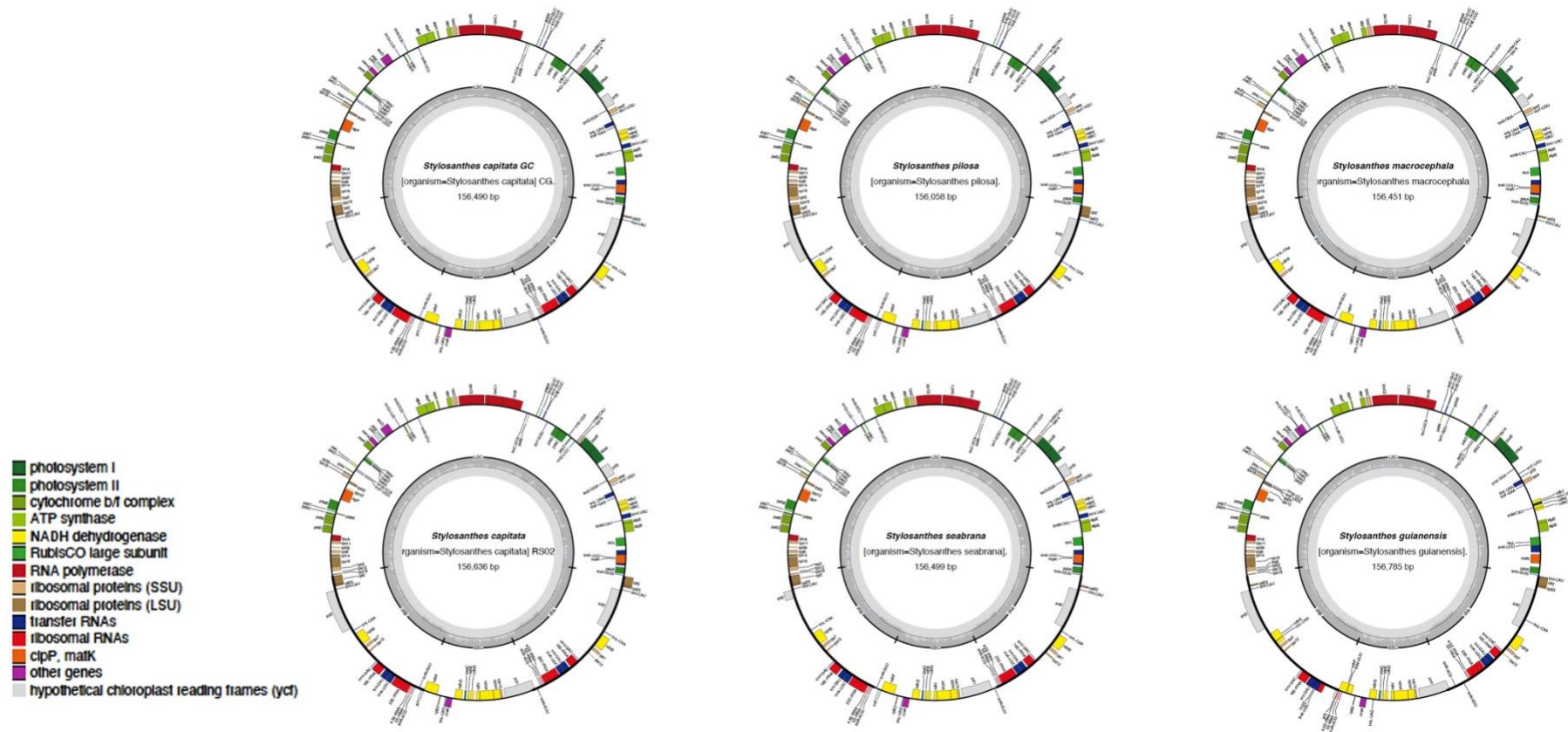


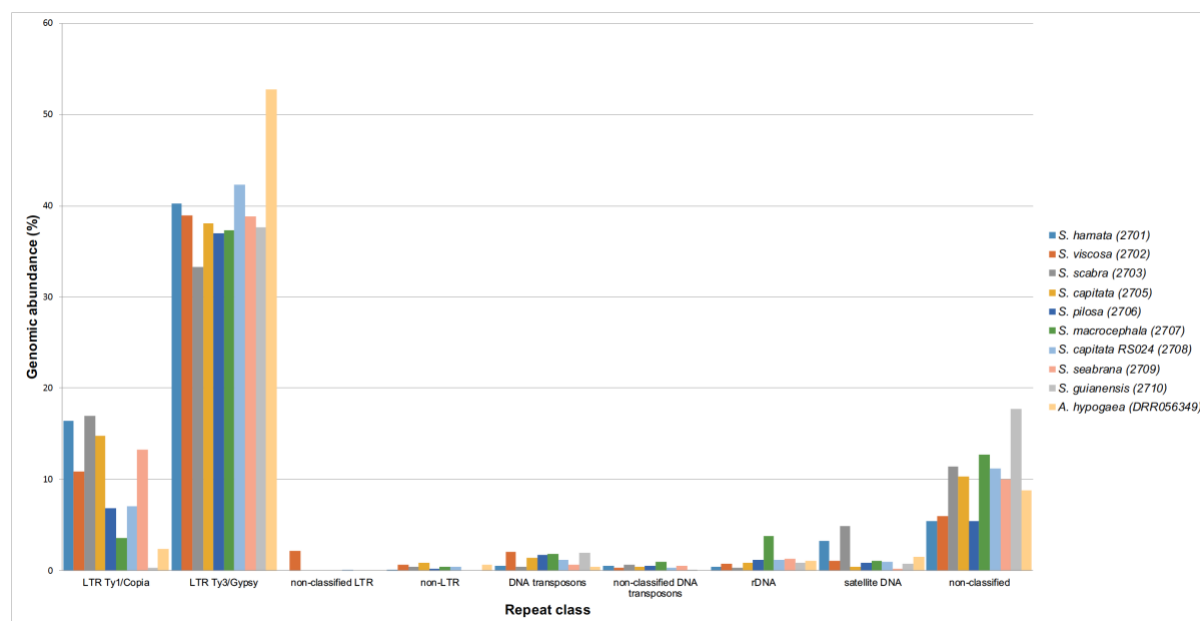
Supplementary Figures



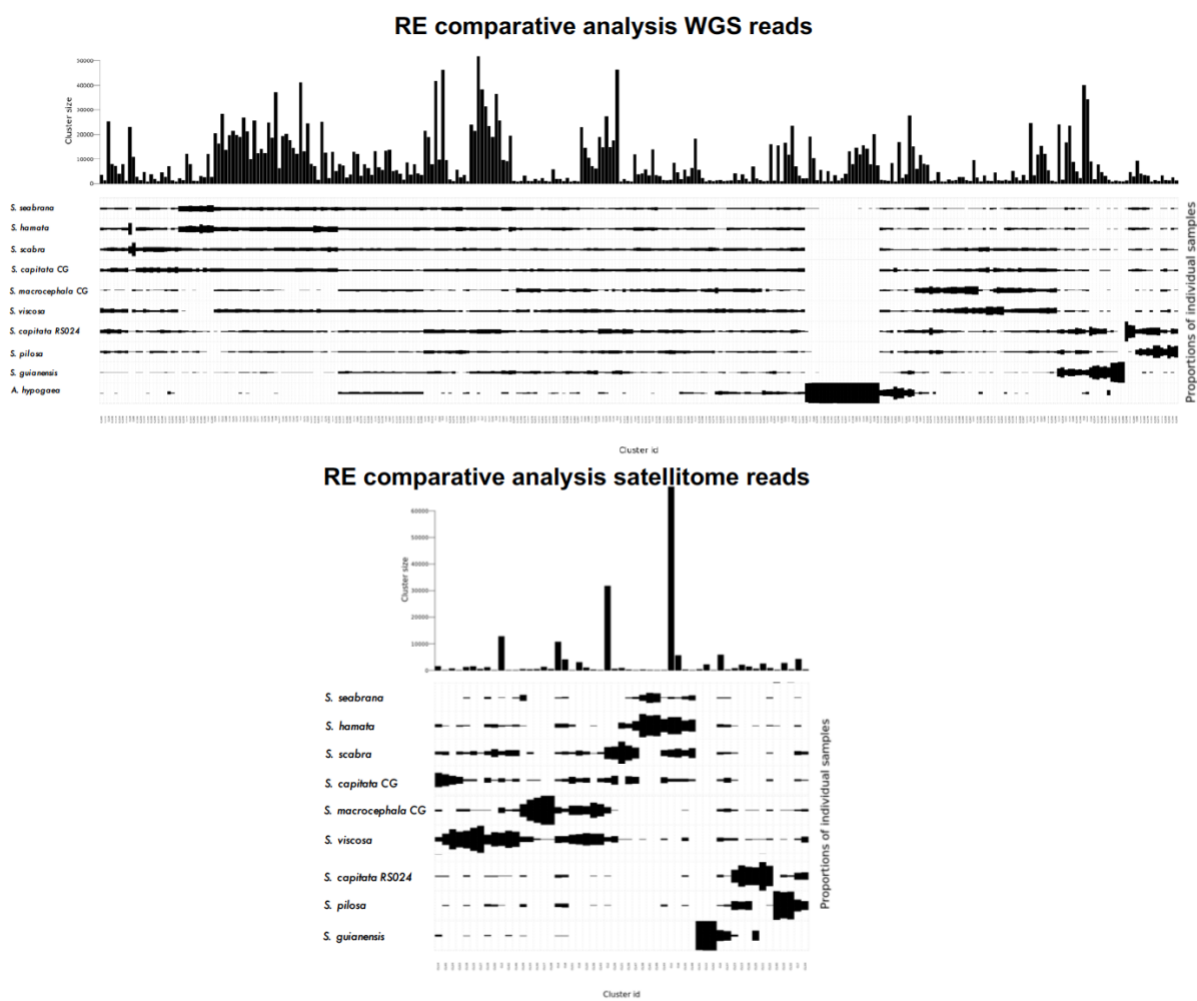
Supplementary Figure 1. Circular gene maps of newly generated mitogenomes for *Stylosanthes hamata*, *S. viscosa*, *S. scabra*, *S. capitata* cv. Campo Grande, *S. pilosa*, *S. macrocephala*, *S. capitata* R3024, *S. seabrana* and *S. guianensis*. Genes on the inside of outer circles are transcribed in a clockwise direction, while genes on the outside of outer circles are transcribed in a reverse direction.



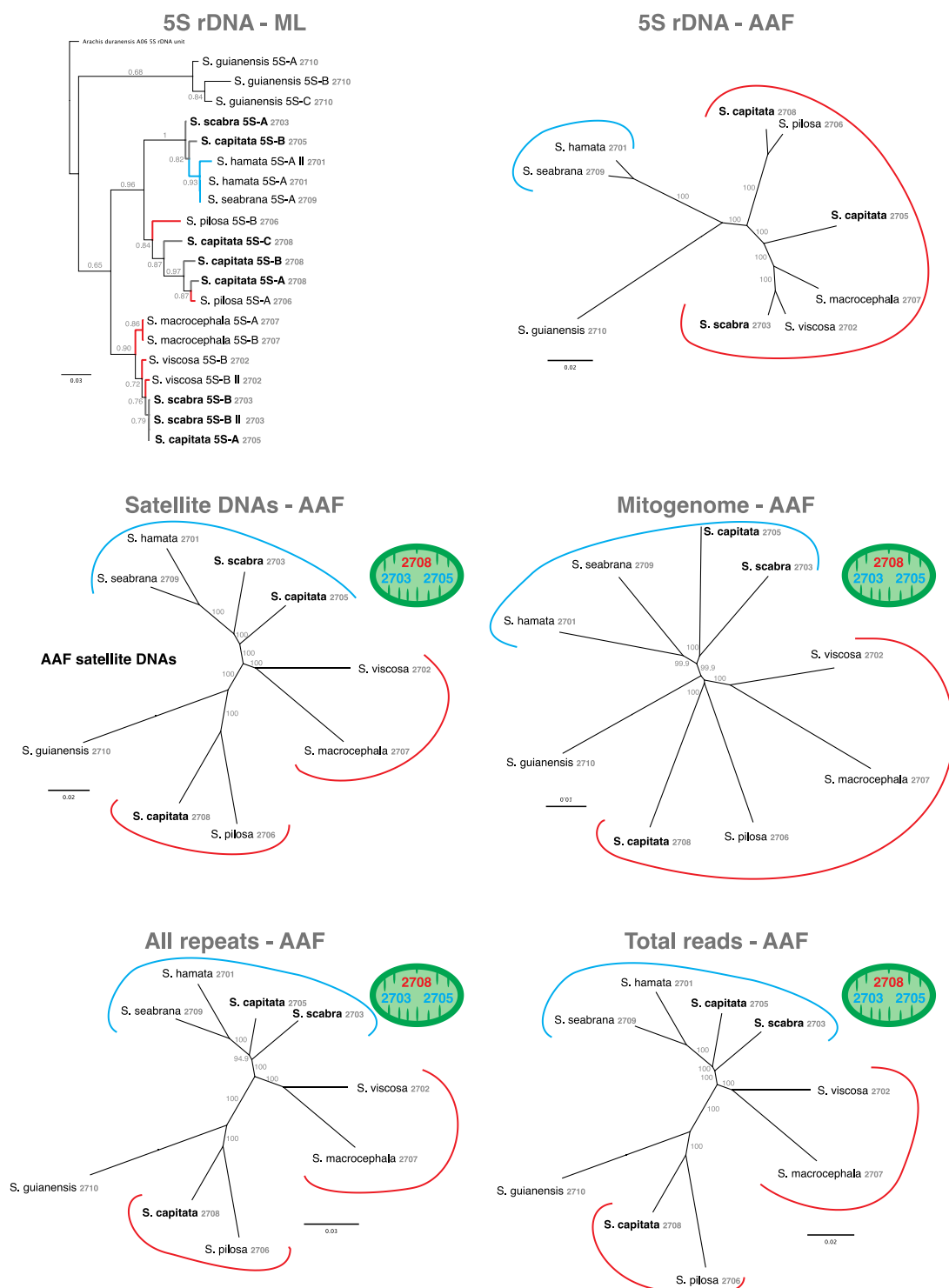
Supplementary Figure 2. Circular gene maps of newly generated plastomes for *S. capitata* cv. Campo Grande, *S. pilosa*, *S. macrocephala*, *S. capitata* RS024, *S. seabrana* and *S. guianensis*. Genic groups are related with colors. Limits of regions LSC, IRa, IRb and SSC are indicated in the inner circle.



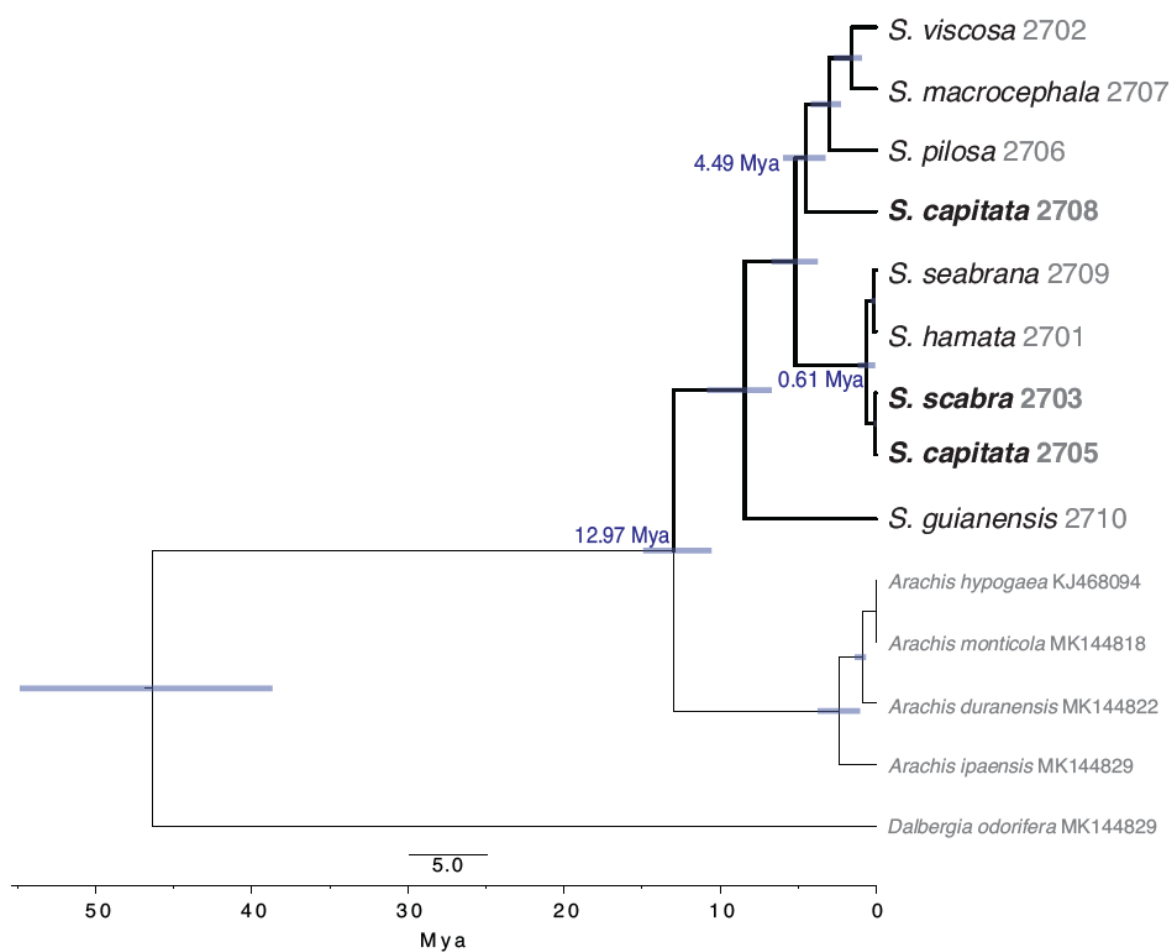
Supplementary Figure 3. Comparative analysis of the main classes of repeats in *Stylosanthes*.



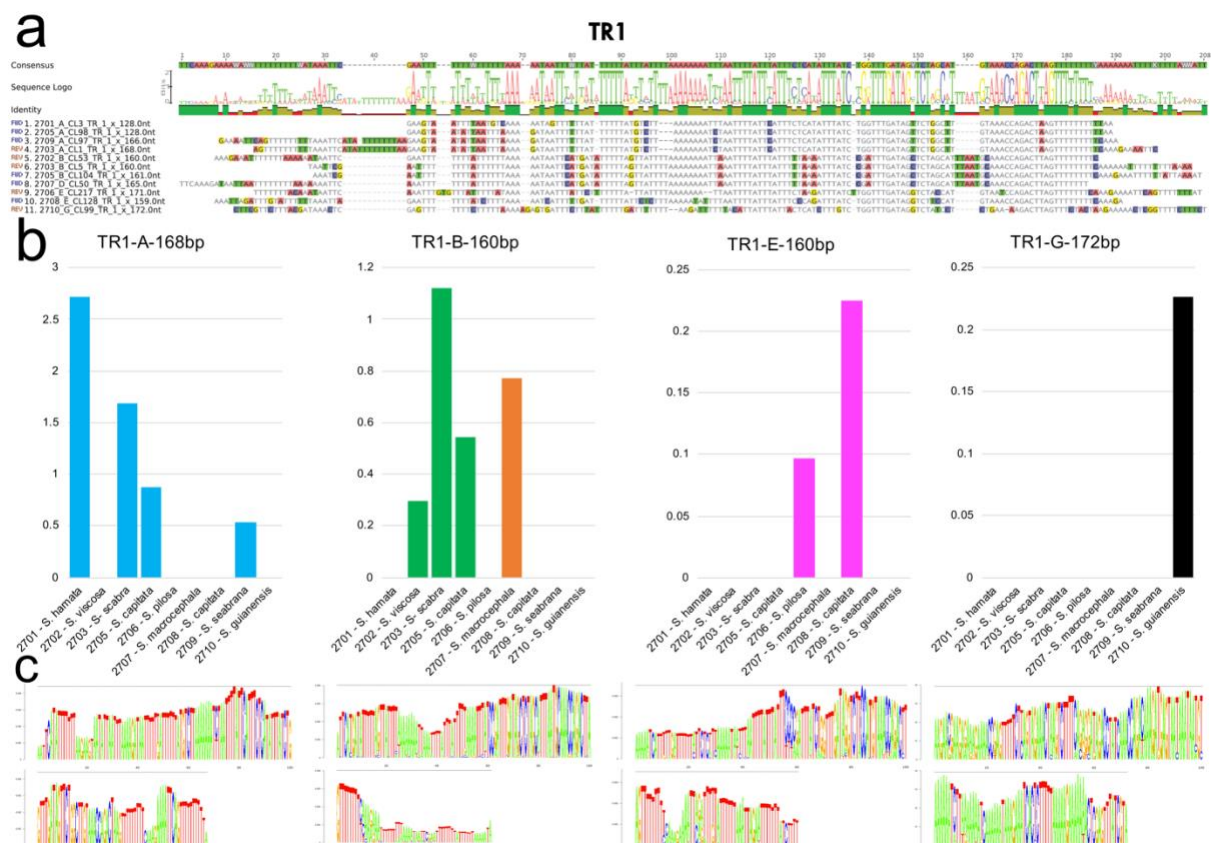
Supplementary Figure 4. Comparative RE2 analysis showing the cumulative abundance across each repeat cluster. Note that both total repeat and satellitome abundance matches species phylogenetic relationships.



Supplementary Figure 5. Alignment-based and AAF phylogenies of different datasets including *Stylosanthes* allopolyploids.



Supplementary Figure 6. A dated Bayesian phylogeny of *Stylosanthes* showing the estimated origin times for allopolyploids.



Supplementary Figure 7. Characterization of TR1, the main family of satellite DNA in *Stylosanthes*. (a) Alignment of the consensus sequences of TR1 extracted from all *Stylosanthes* species analyzed. (b) Genomic abundance of each TR1 variant across all *Stylosanthes* species. (c) Sequence logo of each TR1 variant showing the base-per-base sequence variability found.